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Resequencing 991 rapeseed genomes from a world-wide collection reveals genetic basis of ecotype divergence: A powerful platform for GWAS on agronomic and quality traits

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We report the first pattern of genetic polymorphisms of rapeseed by resequencing a world-wide collection of 991 germplasm accessions. A total of 5.56 or 5.53 million single nucleotide polymorphisms (SNPs) and 1.86 or 1.92 million InDels were identified by mapping reads to the reference genomes of 'Darmor-bzh' or 'Tapidor', respectively. We generated allelic drifting paths that show splits and mixtures of the main populations. The genetic diversity and linkage disequilibrium parameters indicate an asymmetric evolution of the two subgenomes of *B. napus*. The selective-sweep analysis revealed genetic changes in genes orthologous to those regulating various aspects of plant development and response to stresses. Further genome-wide association study identified a variety of SNPs that correspond to flowering time divergence, leaf hairs formation, and seed nutritional quality traits. Our study provides important insights into genomic footprints of the evolution of rapeseed and a powerful GWAS platform for unveiling the genetic control of various agronomic and seed quality traits. We uploaded by far the largest genetic resources for screening of molecular markers for genetic improvement of rapeseed in public domain.

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